Class_09_Mini_Project

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To get started let's read the data!

```r
#we tell R what file we want here
fna.data <- "WisconsinCancer.csv"

#making sure to format the data correctly
wisc.df <- read.csv(fna.data, row.names=1)

#finally let's view our data
head(wisc.df)
```

```
##          diagnosis radius_mean texture_mean perimeter_mean area_mean
## 842302           M       17.99        10.38         122.80    1001.0
## 842517           M       20.57        17.77         132.90    1326.0
## 84300903         M       19.69        21.25         130.00    1203.0
## 84348301         M       11.42        20.38          77.58     386.1
## 84358402         M       20.29        14.34         135.10    1297.0
## 843786           M       12.45        15.70          82.57     477.1
##          smoothness_mean compactness_mean concavity_mean concave.points_mean
## 842302           0.11840          0.27760         0.3001             0.14710
## 842517           0.08474          0.07864         0.0869             0.07017
## 84300903         0.10960          0.15990         0.1974             0.12790
## 84348301         0.14250          0.28390         0.2414             0.10520
## 84358402         0.10030          0.13280         0.1980             0.10430
## 843786           0.12780          0.17000         0.1578             0.08089
##          symmetry_mean fractal_dimension_mean radius_se texture_se perimeter_se
## 842302          0.2419                0.07871    1.0950     0.9053        8.589
## 842517          0.1812                0.05667    0.5435     0.7339        3.398
## 84300903        0.2069                0.05999    0.7456     0.7869        4.585
## 84348301        0.2597                0.09744    0.4956     1.1560        3.445
## 84358402        0.1809                0.05883    0.7572     0.7813        5.438
## 843786          0.2087                0.07613    0.3345     0.8902        2.217
##          area_se smoothness_se compactness_se concavity_se concave.points_se
## 842302    153.40      0.006399        0.04904      0.05373           0.01587
## 842517     74.08      0.005225        0.01308      0.01860           0.01340
## 84300903   94.03      0.006150        0.04006      0.03832           0.02058
## 84348301   27.23      0.009110        0.07458      0.05661           0.01867
## 84358402   94.44      0.011490        0.02461      0.05688           0.01885
## 843786     27.19      0.007510        0.03345      0.03672           0.01137
##          symmetry_se fractal_dimension_se radius_worst texture_worst
## 842302       0.03003             0.006193        25.38         17.33
## 842517       0.01389             0.003532        24.99         23.41
## 84300903     0.02250             0.004571        23.57         25.53
## 84348301     0.05963             0.009208        14.91         26.50
## 84358402     0.01756             0.005115        22.54         16.67
## 843786       0.02165             0.005082        15.47         23.75
##          perimeter_worst area_worst smoothness_worst compactness_worst
## 842302            184.60     2019.0           0.1622            0.6656
## 842517            158.80     1956.0           0.1238            0.1866
## 84300903          152.50     1709.0           0.1444            0.4245
## 84348301           98.87      567.7           0.2098            0.8663
## 84358402          152.20     1575.0           0.1374            0.2050
## 843786            103.40      741.6           0.1791            0.5249
##          concavity_worst concave.points_worst symmetry_worst
## 842302            0.7119               0.2654         0.4601
## 842517            0.2416               0.1860         0.2750
## 84300903          0.4504               0.2430         0.3613
## 84348301          0.6869               0.2575         0.6638
## 84358402          0.4000               0.1625         0.2364
## 843786            0.5355               0.1741         0.3985
##          fractal_dimension_worst
## 842302                   0.11890
## 842517                   0.08902
## 84300903                 0.08758
## 84348301                 0.17300
## 84358402                 0.07678
## 843786                   0.12440
```

When we look at our data so far, we realize that we don't wnat the first row which tells us right away if something is malignant or benign.

```
# We can use -1 here to remove the first column
wisc.data <- wisc.df[,-1]
```

```
# Create diagnosis vector for later
diagnosis <- as.factor(wisc.df$diagnosis)
```

Let's move onto the questions!

> Q1. How many observations are in this dataset?

```
#here we read all the data (minus the first diagnosis column)
dim(wisc.data)
```

```
## [1] 569  30
```

There are 569 rows (or different biopsies to analyze). Each biopsy has 30 elements to it (30 rows).

> Q2. How many of the observations have a malignant diagnosis?

```
#here we can use our diagnosis vector to see how many malignant, or "M" results we have
length(grep(pattern = "M", x = diagnosis))
```

```
## [1] 212
```

There are 212 malignant results in this data set (out of 569 biopsies)

> Q3. How many variables/features in the data are suffixed with _mean?

```
#first we have to be able to read the column names
features <- colnames(wisc.df)
length(grep(pattern = "_mean", x = features))
```

```
## [1] 10
```

There are 10 variables with "_mean" in the variable name.

Performing PCA

```
# Check column means and standard deviations
colMeans(wisc.data)
```

```
##             radius_mean            texture_mean          perimeter_mean
##            1.412729e+01            1.928965e+01            9.196903e+01
##               area_mean         smoothness_mean        compactness_mean
##            6.548891e+02            9.636028e-02            1.043410e-01
##          concavity_mean     concave.points_mean           symmetry_mean
##            8.879932e-02            4.891915e-02            1.811619e-01
##  fractal_dimension_mean               radius_se              texture_se
##            6.279761e-02            4.051721e-01            1.216853e+00
##            perimeter_se                 area_se           smoothness_se
##            2.866059e+00            4.033708e+01            7.040979e-03
##          compactness_se            concavity_se       concave.points_se
##            2.547814e-02            3.189372e-02            1.179614e-02
##             symmetry_se    fractal_dimension_se            radius_worst
##            2.054230e-02            3.794904e-03            1.626919e+01
##           texture_worst         perimeter_worst              area_worst
##            2.567722e+01            1.072612e+02            8.805831e+02
##        smoothness_worst       compactness_worst         concavity_worst
##            1.323686e-01            2.542650e-01            2.721885e-01
##    concave.points_worst          symmetry_worst fractal_dimension_worst
##            1.146062e-01            2.900756e-01            8.394582e-02
```

```
apply(wisc.data,2,sd)
```

```
##             radius_mean            texture_mean          perimeter_mean
##            3.524049e+00            4.301036e+00            2.429898e+01
##               area_mean         smoothness_mean        compactness_mean
##            3.519141e+02            1.406413e-02            5.281276e-02
##          concavity_mean     concave.points_mean           symmetry_mean
##            7.971981e-02            3.880284e-02            2.741428e-02
##  fractal_dimension_mean               radius_se              texture_se
##            7.060363e-03            2.773127e-01            5.516484e-01
##            perimeter_se                 area_se           smoothness_se
##            2.021855e+00            4.549101e+01            3.002518e-03
##          compactness_se            concavity_se       concave.points_se
##            1.790818e-02            3.018606e-02            6.170285e-03
##             symmetry_se    fractal_dimension_se            radius_worst
##            8.266372e-03            2.646071e-03            4.833242e+00
##           texture_worst         perimeter_worst              area_worst
##            6.146258e+00            3.360254e+01            5.693570e+02
##        smoothness_worst       compactness_worst         concavity_worst
##            2.283243e-02            1.573365e-01            2.086243e-01
##    concave.points_worst          symmetry_worst fractal_dimension_worst
##            6.573234e-02            6.186747e-02            1.806127e-02
```

Let's execute PCA now

```
# Perform PCA on wisc.data by completing the following code
wisc.pr <- prcomp(wisc.data, scale = TRUE)

# Look at summary of results
summary(wisc.pr)
```

```
## Importance of components:
##                           PC1    PC2     PC3     PC4     PC5     PC6     PC7
## Standard deviation     3.6444 2.3857 1.67867 1.40735 1.28403 1.09880 0.82172
## Proportion of Variance 0.4427 0.1897 0.09393 0.06602 0.05496 0.04025 0.02251
## Cumulative Proportion  0.4427 0.6324 0.72636 0.79239 0.84734 0.88759 0.91010
##                            PC8    PC9    PC10   PC11    PC12    PC13    PC14
## Standard deviation     0.69037 0.6457 0.59219 0.5421 0.51104 0.49128 0.39624
## Proportion of Variance 0.01589 0.0139 0.01169 0.0098 0.00871 0.00805 0.00523
## Cumulative Proportion  0.92598 0.9399 0.95157 0.9614 0.97007 0.97812 0.98335
##                           PC15    PC16    PC17    PC18    PC19    PC20   PC21
## Standard deviation     0.30681 0.28260 0.24372 0.22939 0.22244 0.17652 0.1731
## Proportion of Variance 0.00314 0.00266 0.00198 0.00175 0.00165 0.00104 0.0010
## Cumulative Proportion  0.98649 0.98915 0.99113 0.99288 0.99453 0.99557 0.9966
##                           PC22    PC23   PC24    PC25    PC26    PC27    PC28
## Standard deviation     0.16565 0.15602 0.1344 0.12442 0.09043 0.08307 0.03987
## Proportion of Variance 0.00091 0.00081 0.0006 0.00052 0.00027 0.00023 0.00005
## Cumulative Proportion  0.99749 0.99830 0.9989 0.99942 0.99969 0.99992 0.99997
##                           PC29    PC30
## Standard deviation     0.02736 0.01153
## Proportion of Variance 0.00002 0.00000
## Cumulative Proportion  1.00000 1.00000
```

> Q4. From your results, what proportion of the original variance is captured by the first principal components (PC1)?

From our summary above we can see that 44.27% of the variance is captured by PC1

> Q5. How many principal components (PCs) are required to describe at least 70% of the original variance in the data?

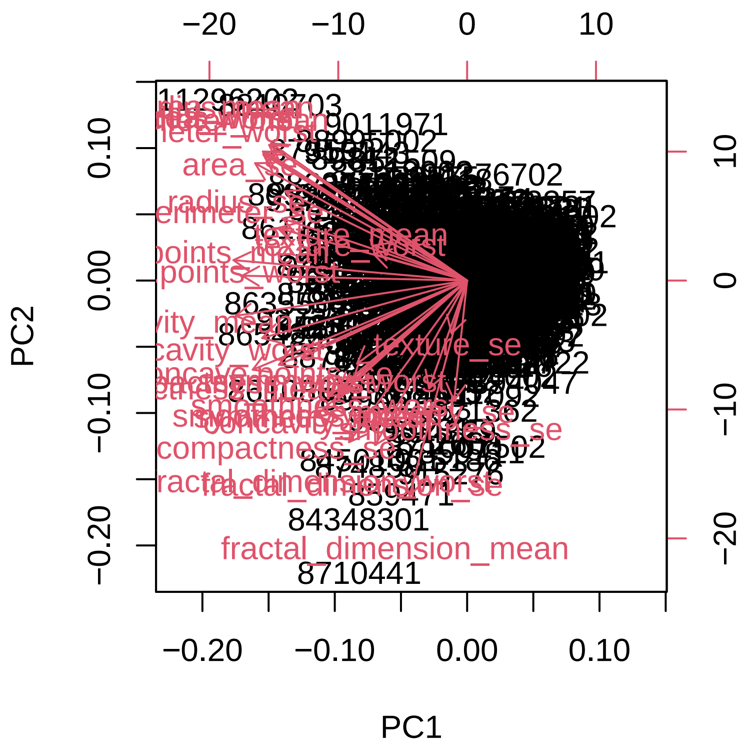
To describe at least 70% of variance, we need 3 principal components

Q6. How many principal components (PCs) are required to describe at least 90% of the original variance in the data?

To describe at least 90% of variance, we need 7 principal components

#Now let's try plotting this out

```
biplot(wisc.pr)
```



```
as.factor(diagnosis)
```

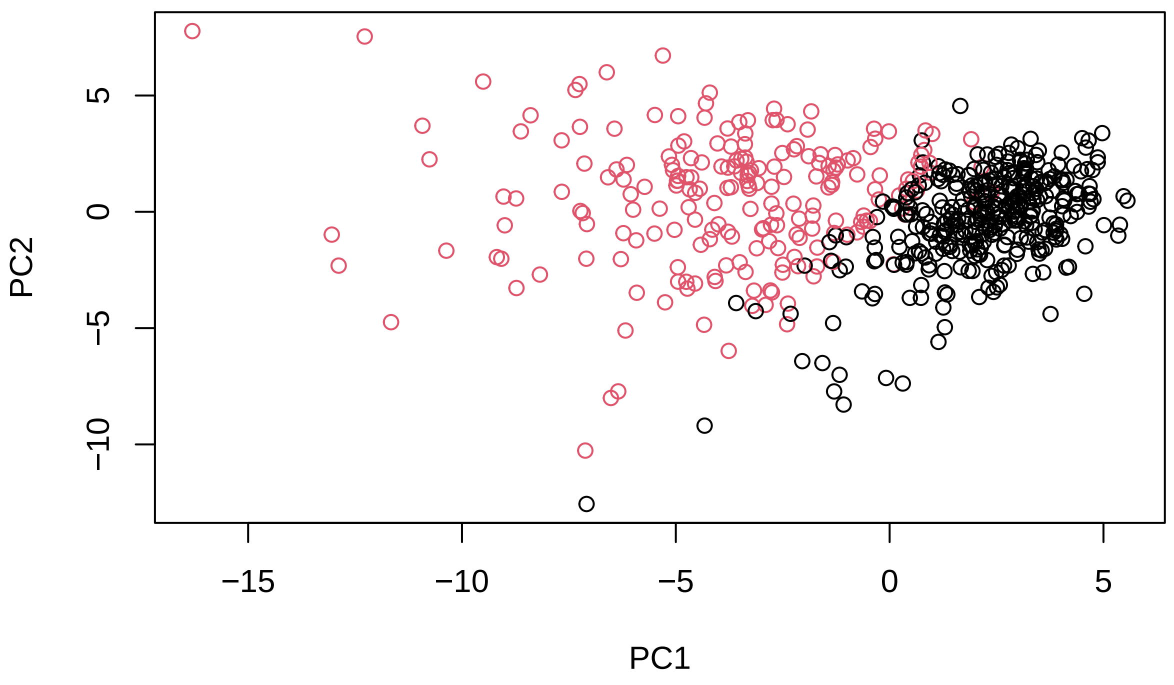
```
##   [1] M M M M M M M M M M M M M M M M M M M B B B M M M M M M M M M M M M M M M
##  [38] B M M M M M M M M B M B B B B B M M B M M B B B B M B M M B B B B M B M M
##  [75] B M B M M B B B M M B M M M B B B M B B M M B B B M M B B B B M B B M B B
## [112] B B B B B B M M M B M M B B B M M B M B M M B M M B B M B B M B B B B M B
## [149] B B B B B B B B M B B B B M M B M B B M M B B M M B B B B M B B M M M B M
## [186] B M B B B M B B M M B M M M M B M M M B M B M B B M B M M M M B B M M B B
## [223] B M B B B B B M M B B M B B M M B M B B B B M B B B B B M B M M M M M M M
## [260] M M M M M M M B B B B B B M B M B B M B B M B M M B B B B B B B B B B B B
## [297] B M B B M B M B B B B B B B B B B B B M B B B M B M B B B B M M M B B
## [334] B B M B M B M B B B M B B B B B B B M M M B B B B B B B B B B B M M B M M
## [371] M B M M B B B B B M B B B B B M B B B M B B M M B B B B B B M B B B B B B
## [408] B M B B B B B M B B M B B B B B B B B B B B B M B M M B M B B B B B M B B
## [445] M B M B B M B M B B B B B B B B M M B B B B B B M B B B B B B B B B B M B
## [482] B B B B B B M B M B B M B B B B B M M B M B M B B B B B M B B M B M B M M
## [519] B B B M B B B B B B B B B B B M B M M B B B B B B B B B B B B B B B B B B
## [556] B B B B B B B M M M M M M B
## Levels: B M
```

Q7. What stands out to you about this plot? Is it easy or difficult to understand? Why?

It is very messy and unable to be read. Even when we pop it out in the larger browser, there are so many points that it is impossible to really read or understand. Row names are being used as labels which makes it hard to read, considering how many rows we have.

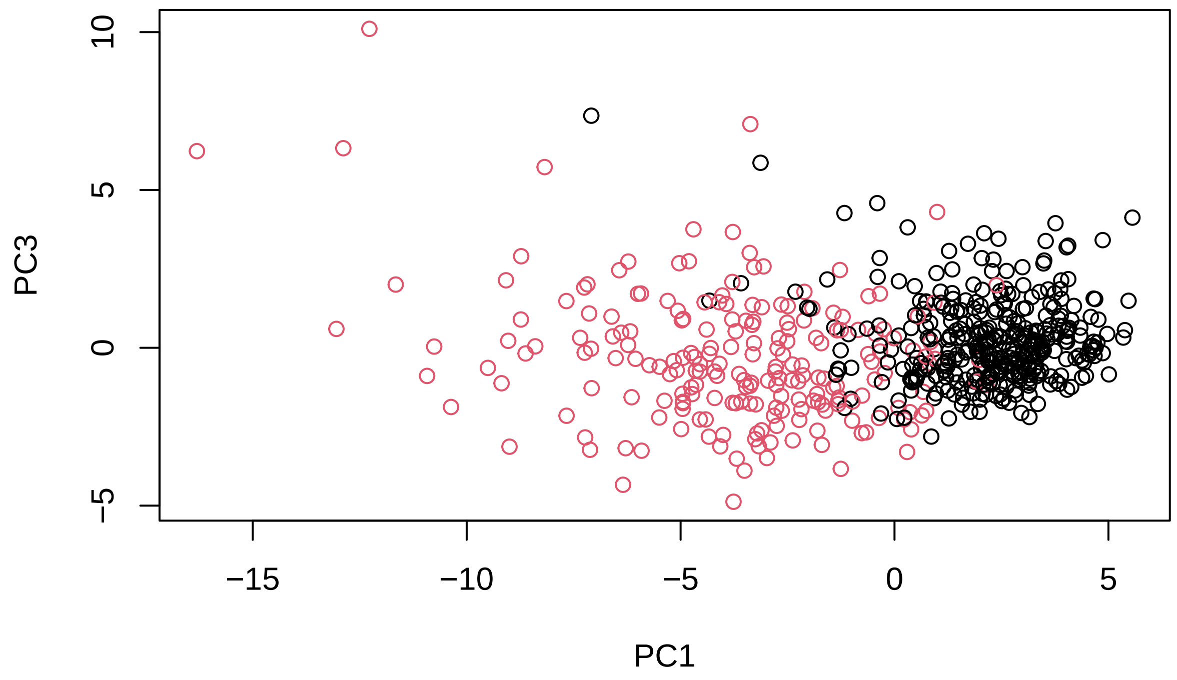
Let's try this again, we are after the score plot (ex: PC1 vs PC2)

```r
# Scatter plot observations by components 1 and 2
plot(wisc.pr$x[,1:2], col = diagnosis ,
     xlab = "PC1", ylab = "PC2")
```



Q8. Generate a similar plot for principal components 1 and 3. What do you notice about these plots?

```r
# Scatter plot observations by components 1 and 3
plot(wisc.pr$x[,1], wisc.pr$x[,3], col = diagnosis ,
     xlab = "PC1", ylab = "PC3")
```

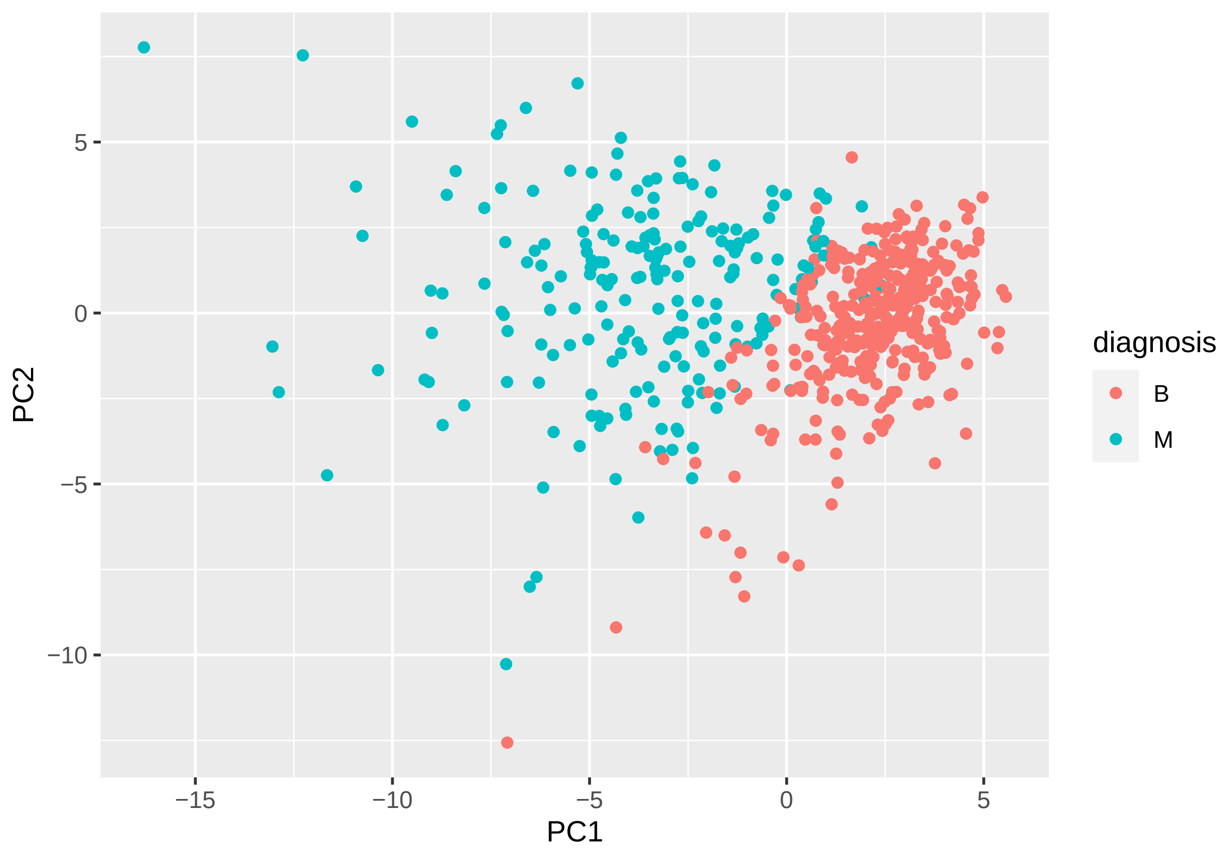


#Now let's try using ggplot to make a nicer looking plot

```
# Create a data.frame for ggplot
df <- as.data.frame(wisc.pr$x)
df$diagnosis <- diagnosis

# Load the ggplot2 package
library(ggplot2)

# Make a scatter plot colored by diagnosis
ggplot(df) +
  aes(PC1, PC2, col = diagnosis) +
  geom_point()
```



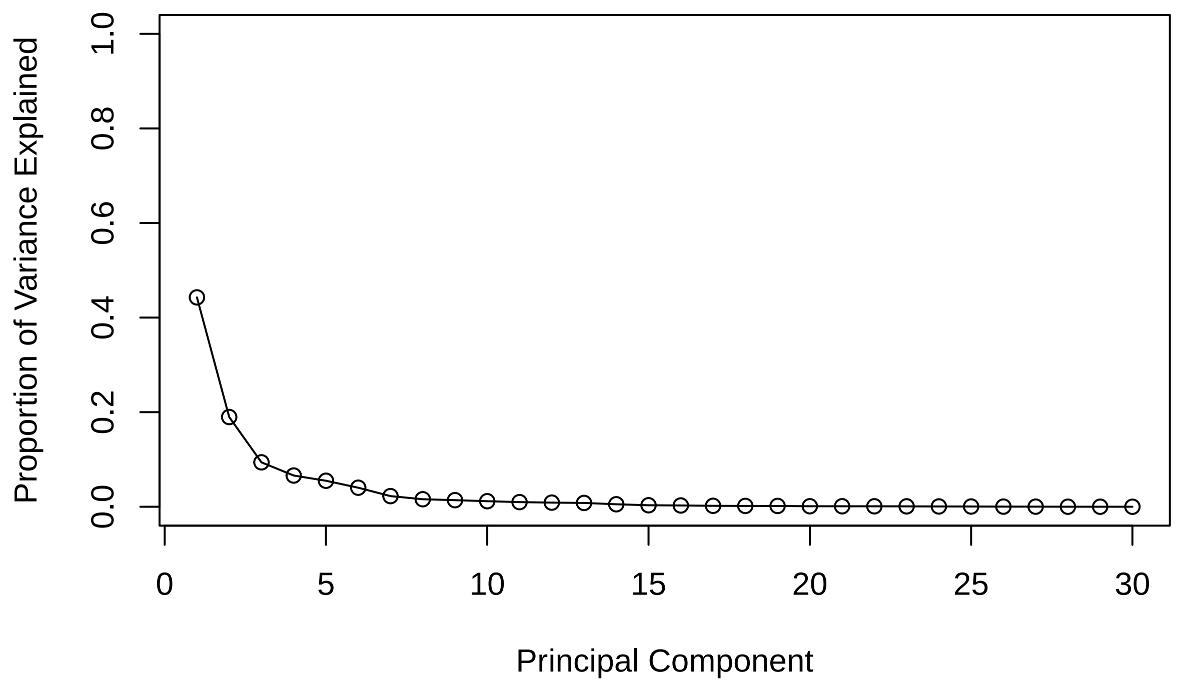
#Variance

```
# Calculate variance of each component
pr.var <- wisc.pr$sdev^2
head(pr.var)
```

```
## [1] 13.281608  5.691355  2.817949  1.980640  1.648731  1.207357
```

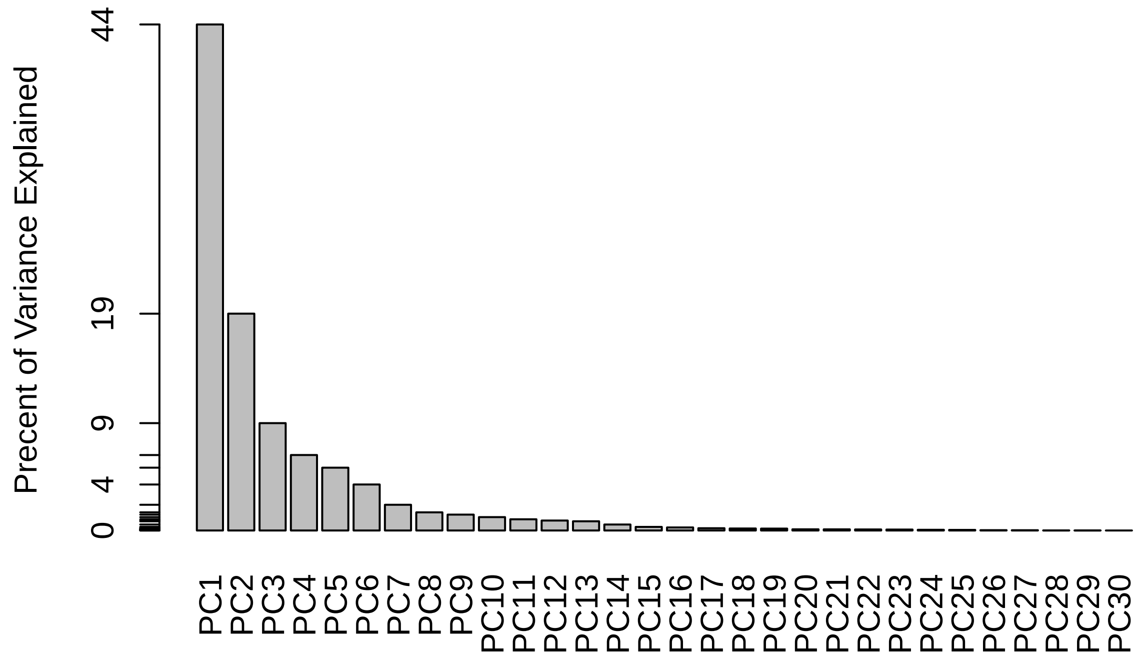
```
# Variance explained by each principal component: pve
pve <- pr.var / sum(pr.var)

# Plot variance explained for each principal component
plot(pve, xlab = "Principal Component",
     ylab = "Proportion of Variance Explained",
     ylim = c(0, 1), type = "o")
```



An alternative graph!

```
# data driven y-axis
barplot(pve, ylab = "Precent of Variance Explained",
     names.arg=paste0("PC",1:length(pve)), las=2, axes = FALSE)
axis(2, at=pve, labels=round(pve,2)*100 )
```



> Q9. For the first principal component, what is the component of the loading vector (i.e. wisc.pr$rotation[,1]) for the feature concave.points_mean?

```
wisc.pr$rotation["concave.points_mean",1]
```

```
## [1] -0.2608538
```

The component of the loading vector for the feature concave.points_mean is -0.26085376.

> Q10. What is the minimum number of principal components required to explain 80% of the variance of the data?

```
var <- summary(wisc.pr)
var$importance[2,]
```

```
##     PC1     PC2     PC3     PC4     PC5     PC6     PC7     PC8     PC9    PC10
## 0.44272 0.18971 0.09393 0.06602 0.05496 0.04025 0.02251 0.01589 0.01390 0.01169
##    PC11    PC12    PC13    PC14    PC15    PC16    PC17    PC18    PC19    PC20
## 0.00980 0.00871 0.00805 0.00523 0.00314 0.00266 0.00198 0.00175 0.00165 0.00104
##    PC21    PC22    PC23    PC24    PC25    PC26    PC27    PC28    PC29    PC30
## 0.00100 0.00091 0.00081 0.00060 0.00052 0.00027 0.00023 0.00005 0.00002 0.00000
```

We need at least 5 principal components to explain 80% variance of the data.

#Hierarchal Clustering

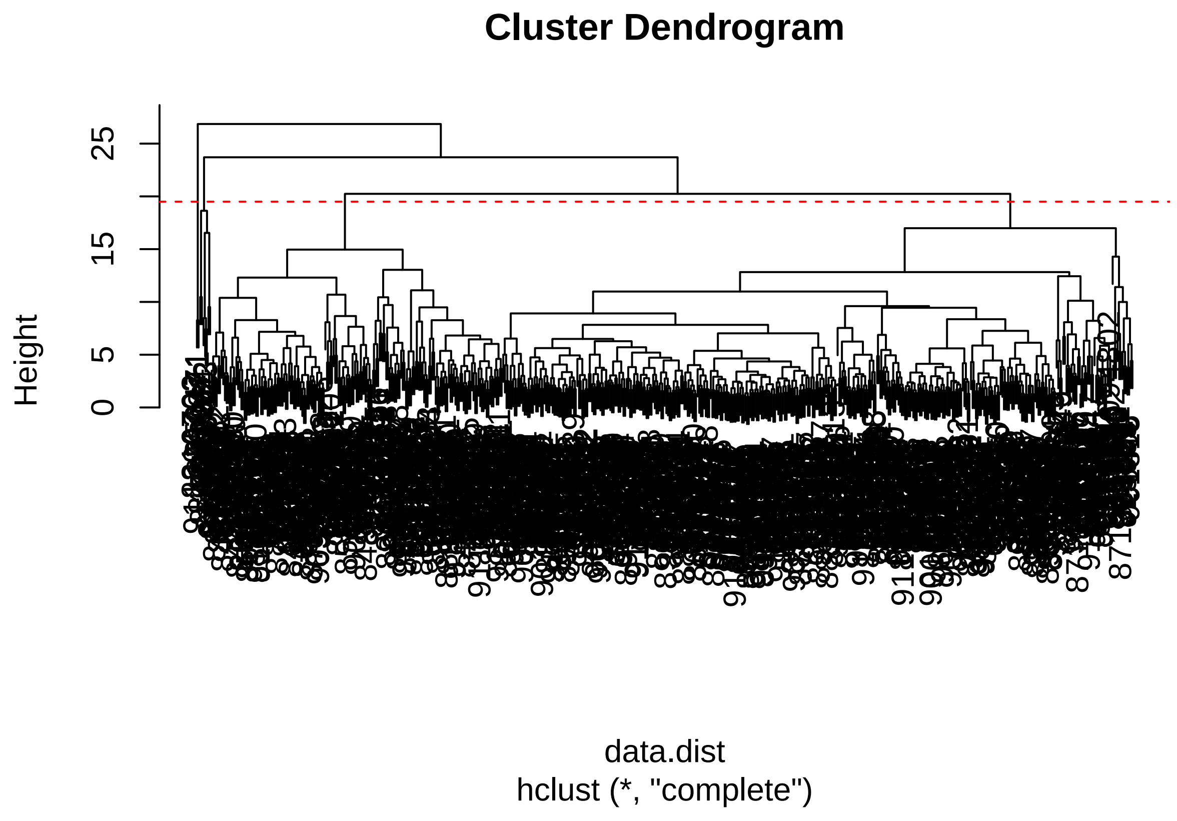
```
# Scale the wisc.data data using the "scale()" function
data.scaled <- scale(wisc.data)
```

```
#Calculate the (Euclidean) distances between all pairs of observations
data.dist <- dist(data.scaled)
```

```
#Create a hierarchical clustering model using complete linkage.
wisc.hclust <- hclust(data.dist, method = "complete")
```

> Q11. Using the plot() and abline() functions, what is the height at which the clustering model has 4 clusters?

```
plot(wisc.hclust)
#not too sure how exactly to calcuate where it cuts off, eyeballed it for now
abline(h = 19.5, col="red", lty=2)
```



#Selecting number of clusters

```
wisc.hclust.clusters <- cutree(wisc.hclust, k = 4)

#We can use the table() function to compare the cluster membership to the actual diagnoses.
table(wisc.hclust.clusters, diagnosis)
```

```
##                         diagnosis
## wisc.hclust.clusters   B   M
##                    1  12 165
##                    2   2   5
##                    3 343  40
##                    4   0   2
```

> Q12. Can you find a better cluster vs diagnoses match by cutting into a different number of clusters between 2 and 10?

```
#Let's try out different cluster groups
wisc.hclust.clusters2 <- cutree(wisc.hclust, k = 2)
table(wisc.hclust.clusters2, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters2   B   M
##                     1 357 210
##                     2   0   2
```

```
wisc.hclust.clusters3 <- cutree(wisc.hclust, k = 3)
table(wisc.hclust.clusters3, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters3   B   M
##                     1 355 205
##                     2   2   5
##                     3   0   2
```

```
wisc.hclust.clusters5 <- cutree(wisc.hclust, k = 5)
table(wisc.hclust.clusters5, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters5   B   M
##                     1  12 165
##                     2   0   5
##                     3 343  40
##                     4   2   0
##                     5   0   2
```

```
wisc.hclust.clusters6 <- cutree(wisc.hclust, k = 6)
table(wisc.hclust.clusters6, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters6   B   M
##                     1  12 165
##                     2   0   5
##                     3 331  39
##                     4   2   0
##                     5  12   1
##                     6   0   2
```

```r
wisc.hclust.clusters7 <- cutree(wisc.hclust, k = 7)
table(wisc.hclust.clusters7, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters7   B   M
##                     1  12 165
##                     2   0   3
##                     3 331  39
##                     4   2   0
##                     5  12   1
##                     6   0   2
##                     7   0   2
```

```r
wisc.hclust.clusters8 <- cutree(wisc.hclust, k = 8)
table(wisc.hclust.clusters8, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters8   B   M
##                     1  12  86
##                     2   0  79
##                     3   0   3
##                     4 331  39
##                     5   2   0
##                     6  12   1
##                     7   0   2
##                     8   0   2
```

```r
wisc.hclust.clusters9 <- cutree(wisc.hclust, k = 9)
table(wisc.hclust.clusters9, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters9   B   M
##                     1  12  86
##                     2   0  79
##                     3   0   3
##                     4 331  39
##                     5   2   0
##                     6  12   0
##                     7   0   2
##                     8   0   2
##                     9   0   1
```

```r
wisc.hclust.clusters10 <- cutree(wisc.hclust, k = 10)
table(wisc.hclust.clusters10, diagnosis)
```

```
##                       diagnosis
## wisc.hclust.clusters10   B   M
##                     1   12  86
##                     2    0  59
##                     3    0   3
##                     4  331  39
##                     5   0  20
##                     6   2   0
##                     7  12   0
##                     8   0   2
##                     9   0   2
##                     10  0   1
```

With 6-10 clusters, the results are almsost exactly the same to one another, we can rule those out.

```
wisc.hclust.clusters2 <- cutree(wisc.hclust, k = 2)
table(wisc.hclust.clusters2, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters2   B   M
##                     1 357 210
##                     2   0   2
```

```
wisc.hclust.clusters3 <- cutree(wisc.hclust, k = 3)
table(wisc.hclust.clusters3, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters3   B   M
##                     1 355 205
##                     2   2   5
##                     3   0   2
```

```
#this is our original
wisc.hclust.clusters <- cutree(wisc.hclust, k = 4)
table(wisc.hclust.clusters, diagnosis)
```

```
##                     diagnosis
## wisc.hclust.clusters   B   M
##                    1  12 165
##                    2   2   5
##                    3 343  40
##                    4   0   2
```

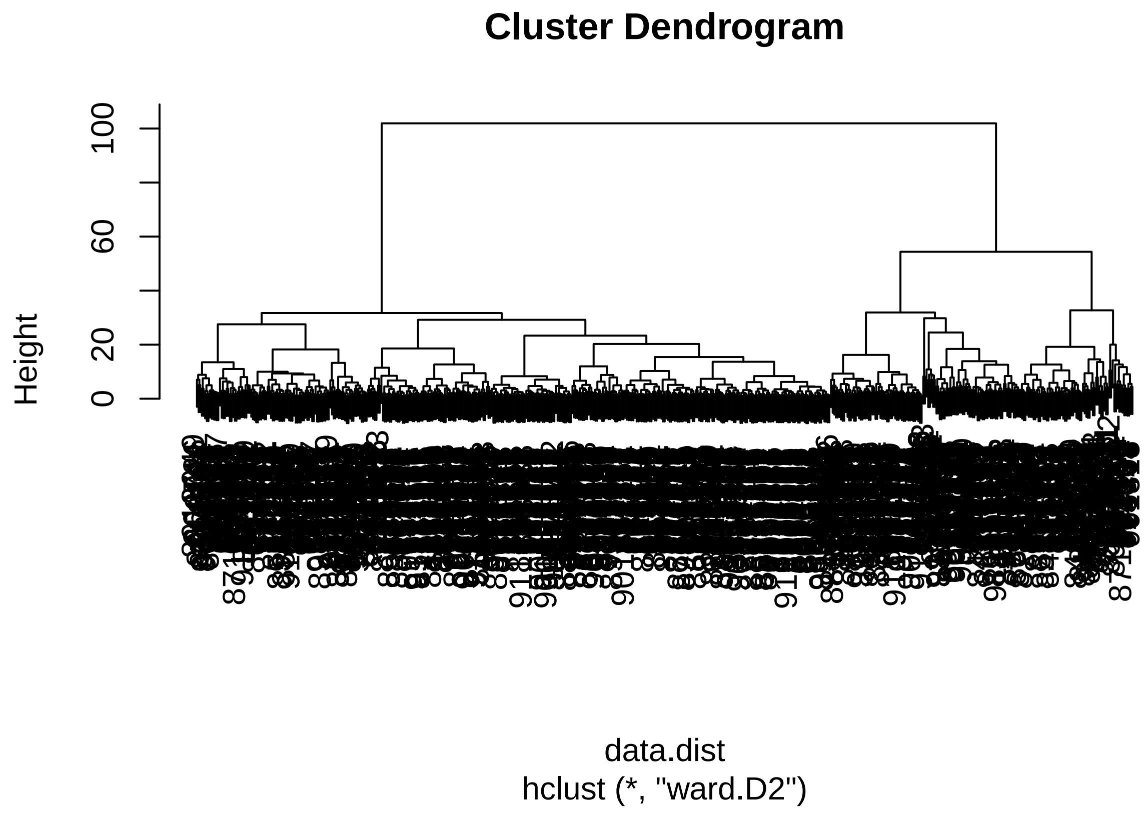
```
wisc.hclust.clusters5 <- cutree(wisc.hclust, k = 5)
table(wisc.hclust.clusters5, diagnosis)
```

```
##                      diagnosis
## wisc.hclust.clusters5   B   M
##                     1  12 165
##                     2   0   5
##                     3 343  40
##                     4   2   0
##                     5   0   2
```

Having 3 clusters gives a better cluster vs. diagnosis match because we can see in this table that cluster 1 represents almost all the data (560/569). We can see here that there are 355 benign cellsa nd 205 malignant ones.

Q13. Which method gives your favorite results for the same data.dist dataset? Explain your reasoning.

```
wisc.hclust13 <- hclust(data.dist, method = "ward.D2")
plot(wisc.hclust13)
```



This gives 3 clusters, like we decided on in the previous question. This gives us the grouping that we want.

#Combining Methods

We take the results of our PCA analysis and cluster in this space

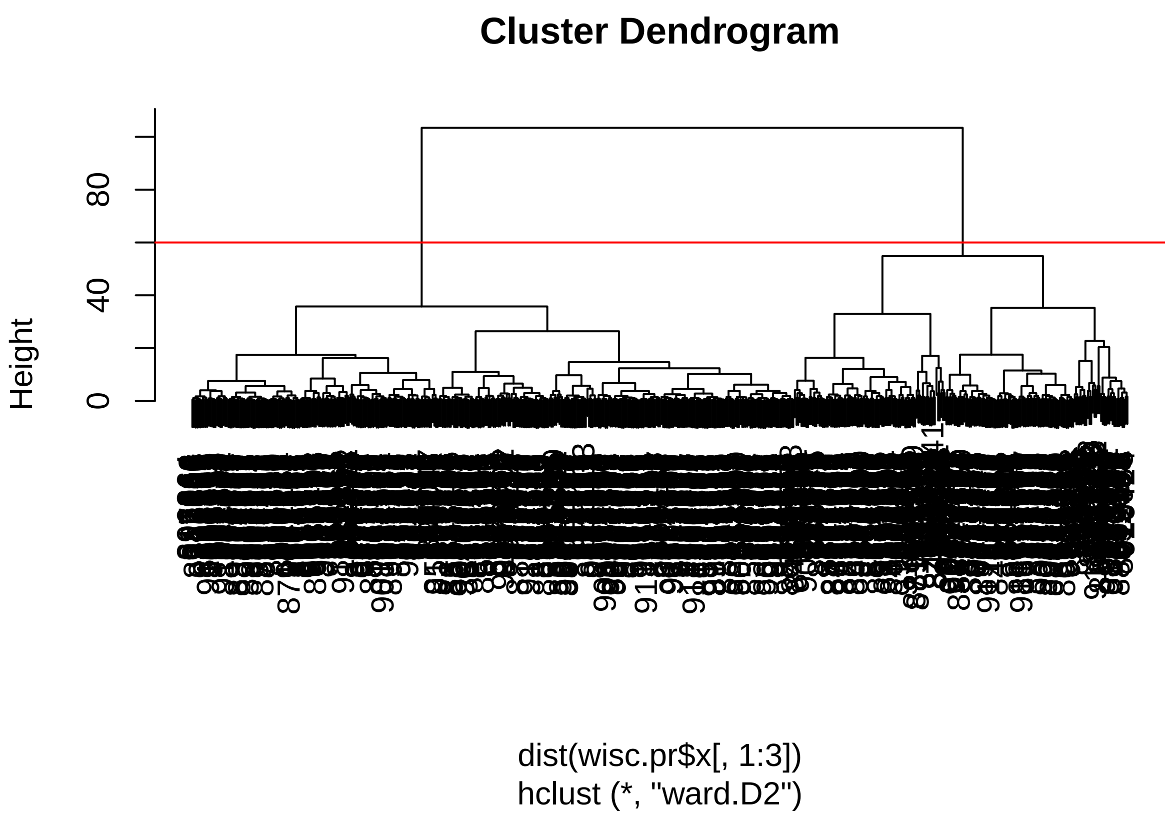
```
summary(wisc.pr)
```

```
## Importance of components:
##                           PC1    PC2     PC3     PC4     PC5     PC6     PC7
## Standard deviation     3.6444 2.3857 1.67867 1.40735 1.28403 1.09880 0.82172
## Proportion of Variance 0.4427 0.1897 0.09393 0.06602 0.05496 0.04025 0.02251
## Cumulative Proportion  0.4427 0.6324 0.72636 0.79239 0.84734 0.88759 0.91010
##                            PC8    PC9    PC10   PC11    PC12    PC13    PC14
## Standard deviation     0.69037 0.6457 0.59219 0.5421 0.51104 0.49128 0.39624
## Proportion of Variance 0.01589 0.0139 0.01169 0.0098 0.00871 0.00805 0.00523
## Cumulative Proportion  0.92598 0.9399 0.95157 0.9614 0.97007 0.97812 0.98335
##                           PC15    PC16    PC17    PC18    PC19    PC20   PC21
## Standard deviation     0.30681 0.28260 0.24372 0.22939 0.22244 0.17652 0.1731
## Proportion of Variance 0.00314 0.00266 0.00198 0.00175 0.00165 0.00104 0.0010
## Cumulative Proportion  0.98649 0.98915 0.99113 0.99288 0.99453 0.99557 0.9966
##                           PC22    PC23   PC24    PC25    PC26    PC27    PC28
## Standard deviation     0.16565 0.15602 0.1344 0.12442 0.09043 0.08307 0.03987
## Proportion of Variance 0.00091 0.00081 0.0006 0.00052 0.00027 0.00023 0.00005
## Cumulative Proportion  0.99749 0.99830 0.9989 0.99942 0.99969 0.99992 0.99997
##                           PC29    PC30
## Standard deviation     0.02736 0.01153
## Proportion of Variance 0.00002 0.00000
## Cumulative Proportion  1.00000 1.00000
```

```
#First we have to create something with at least 90% of variance explained for
wisc.pr.hclust <- hclust(dist(wisc.pr$x[,1:3] ),
                         method = "ward.D2")
```

Plotting the dendeogram

```
plot(wisc.pr.hclust)
abline(h=60, col="red")
```



Cut the tree into k=2 groups

```
grps <- cutree(wisc.pr.hclust, k=2)
table(grps)
```

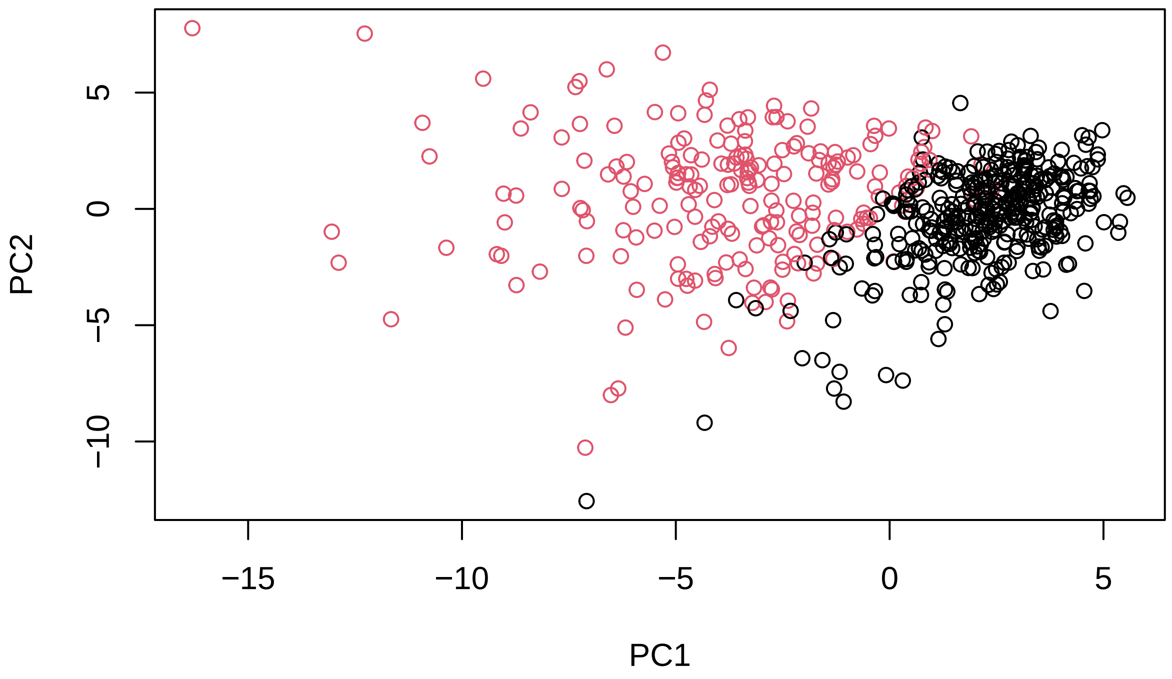
```
## grps
##   1   2
## 203 366
```

Cross table compare of diagnosis and my cluster groups

```
table(diagnosis, grps)
```

```
##          grps
## diagnosis   1   2
##         B  24 333
##         M 179  33
```

```
plot(wisc.pr$x[,1:2], col=diagnosis)
```



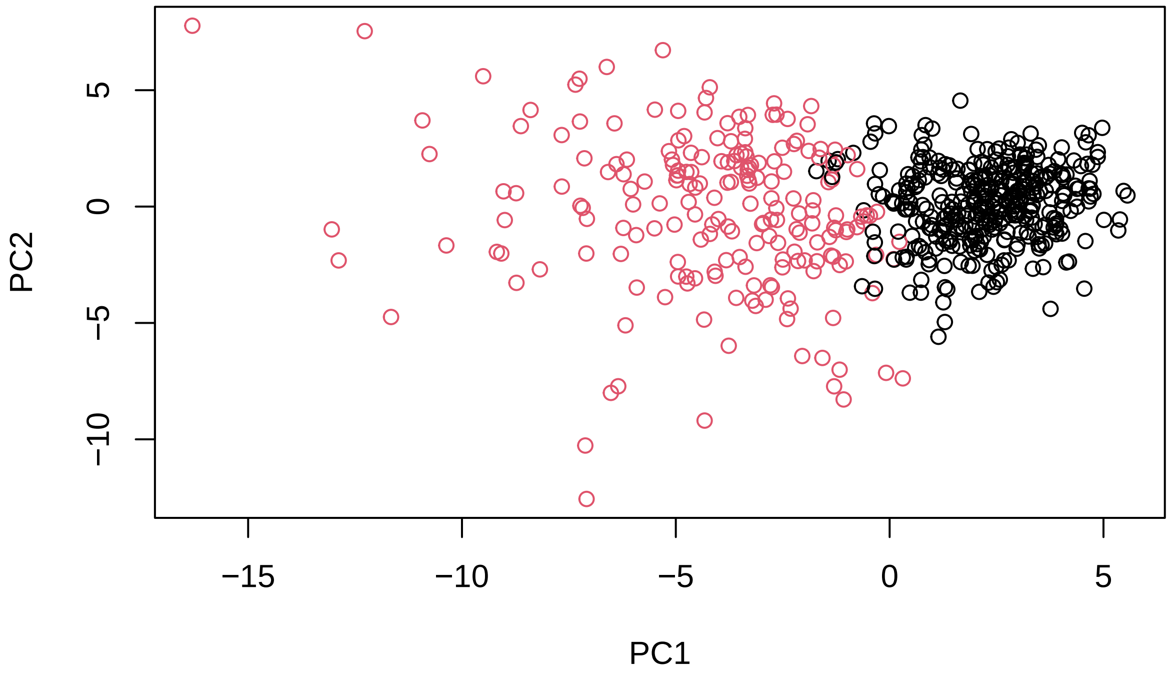
```
g <- as.factor(grps)
levels(g)
```

```
## [1] "1" "2"
```

```
g <- relevel(g,2)
levels(g)
```

```
## [1] "2" "1"
```

```r
# Plot using our re-ordered factor
plot(wisc.pr$x[,1:2], col=g)
```



```r
## Use the distance along the first 7 PCs for clustering i.e. wisc.pr$x[, 1:7]
wisc.pr.hclust <- hclust(dist(wisc.pr$x[,1:7] ),
                         method = "ward.D2")
```

```r
wisc.pr.hclust.clusters <- cutree(wisc.pr.hclust, k=2)
```

Q15. How well does the newly created model with four clusters separate out the two diagnoses?

```r
# Compare to actual diagnoses
table(wisc.pr.hclust.clusters, diagnosis)
```

```
##                          diagnosis
## wisc.pr.hclust.clusters   B   M
##                       1  28 188
##                       2 329  24
```

The newly created model sorts once again benign/malignant tumors pretty well. A little better than our previous sorting but honestly still pretty similar.

Q16. How well do the k-means and hierarchical clustering models you created in previous sections (i.e. before PCA) do in terms of separating the diagnoses? Again, use the table() function to compare the output of each model (wisc.km$cluster and wisc.hclust.clusters) with the vector containing the actual diagnoses.

```
#this was from the optional part 4 but have to create a wisc.km
wisc.km <- kmeans(wisc.data, centers= 2, nstart= 20)

table(wisc.km$cluster, diagnosis)
```

```
##    diagnosis
##       B   M
##   1   1 130
##   2 356  82
```

```
table(wisc.hclust.clusters, diagnosis)
```

```
##                     diagnosis
## wisc.hclust.clusters   B   M
##                    1  12 165
##                    2   2   5
##                    3 343  40
##                    4   0   2
```

From our wisc.hclust.clusters (hierarchal) data, we can see that there are more clusters (4), and provide mostly better results of malignant vs benign. Cluster 1 has 12/165 showing benigb, cluster 3 has 343/383 showing benign, and cluster 4 has 2/2 showing malignant. These results could lead to less false positives. But cluster 3 shows 2/7 as benign, this one cluster is not as defined (in terms of malignant vs. benign).

For our k-means, we have 2 clusters with pretty good separation of benign vs. malignant. Cluster 1 has 130/131 showing to be malignant, and Cluster 2 shows 356/438 to be benign. Personally I think the k-means data is better to look at just as a table, it's Cluster 1 is very accurate.

#Sensitivity/Specificity

> Q17. Which of your analysis procedures resulted in a clustering model with the best specificity? How about sensitivity?

```
#Calculating for sensitivity
130 / (130+82)
```

```
## [1] 0.6132075
```

```
165 / (165+40+5+2)
```

```
## [1] 0.7783019
```

```
#Calculating for Specificity
356 / (356+1)
```

```
## [1] 0.9971989
```

```
343 / (343+12)
```

```
## [1] 0.9661972
```

The use of hierarchal clustering is better for sensitivity

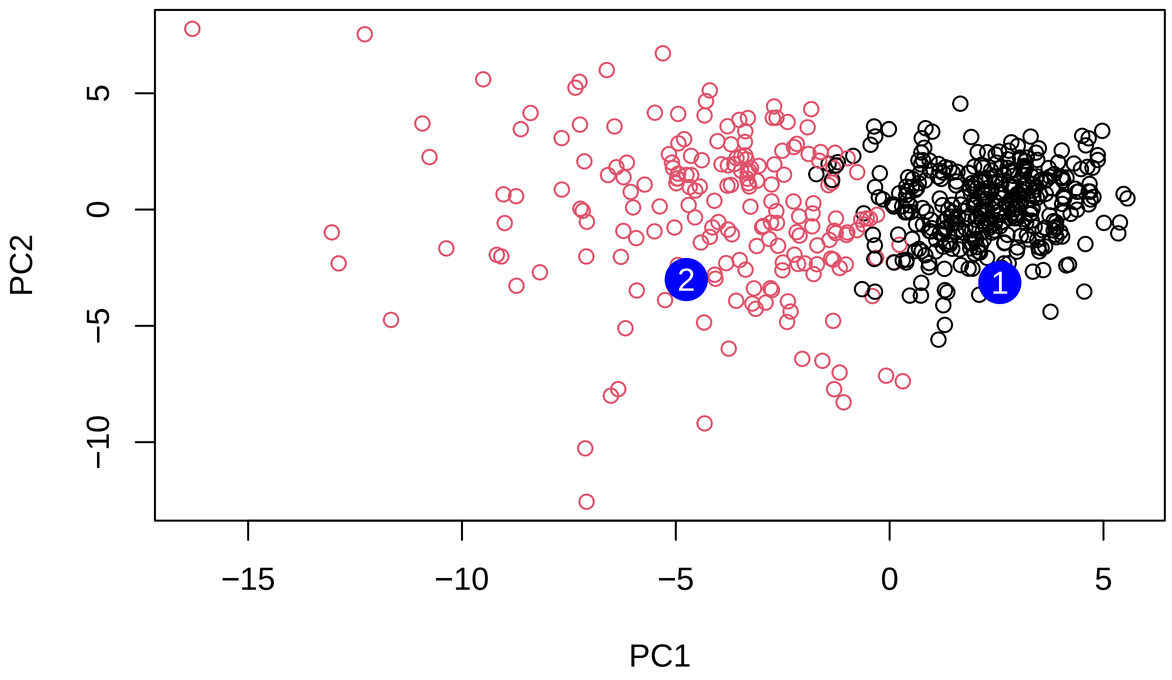
The use of k-means is better for specificity

#Prediction

```
#url <- "new_samples.csv"
url <- "https://tinyurl.com/new-samples-CSV"
new <- read.csv(url)
npc <- predict(wisc.pr, newdata=new)
npc
```

```
##            PC1       PC2        PC3        PC4       PC5        PC6        PC7
## [1,]  2.576616 -3.135913  1.3990492 -0.7631950  2.781648 -0.8150185 -0.3959098
## [2,] -4.754928 -3.009033 -0.1660946 -0.6052952 -1.140698 -1.2189945  0.8193031
##             PC8       PC9       PC10      PC11      PC12      PC13     PC14
## [1,] -0.2307350 0.1029569 -0.9272861 0.3411457  0.375921 0.1610764 1.187882
## [2,] -0.3307423 0.5281896 -0.4855301 0.7173233 -1.185917 0.5893856 0.303029
##           PC15       PC16        PC17        PC18        PC19       PC20
## [1,] 0.3216974 -0.1743616 -0.07875393 -0.11207028 -0.08802955 -0.2495216
## [2,] 0.1299153  0.1448061 -0.40509706  0.06565549  0.25591230 -0.4289500
##            PC21       PC22       PC23       PC24        PC25         PC26
## [1,]  0.1228233 0.09358453 0.08347651  0.1223396  0.02124121  0.078884581
## [2,] -0.1224776 0.01732146 0.06316631 -0.2338618 -0.20755948 -0.009833238
##              PC27        PC28         PC29         PC30
## [1,]  0.220199544 -0.02946023 -0.015620933  0.005269029
## [2,] -0.001134152  0.09638361  0.002795349 -0.019015820
```

```
plot(wisc.pr$x[,1:2], col=g)
points(npc[,1], npc[,2], col="blue", pch=16, cex=3)
text(npc[,1], npc[,2], c(1,2), col="white")
```



Q18. Which of these new patients should we prioritize for follow up based on your results?

We would prioritize patient 2 because their clustering/data looks more like the (mostly) malignant patients (more like cluster 1 which had mostly malignant tumors in our previous Wisconsin data).

```
sessionInfo()
```

```
## R version 4.1.1 (2021-08-10)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] ggplot2_3.3.5
##
## loaded via a namespace (and not attached):
```

```
##  [1] knitr_1.36       magrittr_2.0.1   tidyselect_1.1.1 munsell_0.5.0
##  [5] colorspace_2.0-2 R6_2.5.1         rlang_0.4.11     fastmap_1.1.0
##  [9] fansi_0.5.0      dplyr_1.0.7      stringr_1.4.0    highr_0.9
## [13] tools_4.1.1      grid_4.1.1       gtable_0.3.0     xfun_0.26
## [17] utf8_1.2.2       withr_2.4.2      htmltools_0.5.2  ellipsis_0.3.2
## [21] yaml_2.2.1       digest_0.6.28    tibble_3.1.5     lifecycle_1.0.1
## [25] crayon_1.4.1     farver_2.1.0     purrr_0.3.4      vctrs_0.3.8
## [29] glue_1.4.2       evaluate_0.14    rmarkdown_2.11   labeling_0.4.2
## [33] stringi_1.7.5    compiler_4.1.1   pillar_1.6.3     generics_0.1.0
## [37] scales_1.1.1     pkgconfig_2.0.3
```